

DNA

mcb398

1

1140

Mitochondrial cytochrome b gene (1140 bp)

mcb869

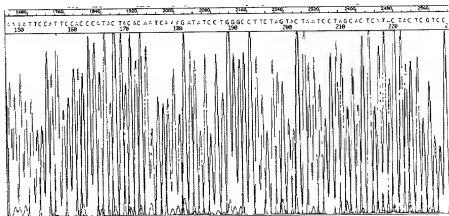
PCR amplicons
(472 bp)

M

500 bp-

72 bp

Sequencing using 'ABI Prism 3700' DNA Analyzer



Revealed sequence (328 bp)

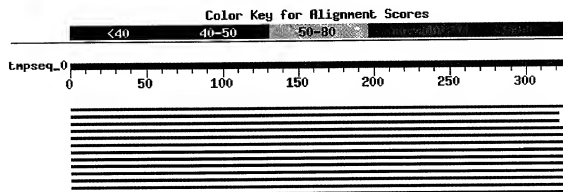
TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCTTGACAC
GATTCTTTGGCTTCCATCTCATCTTCTCATTATCATCTCAGC
TCTAGCAGCAGTCACCTCCTATTCTTTCACGAGCAGGATCT
AACAACCCCTCAGGAATAGTATCCGATCTCAGACAAATTCAT
TCCACCCATACTACACAATCAAAGATATCTGGGCTTCTAGT
ACTAATCTTAGCATCTATACTACTCGTCTATTCTCACCAGAC
CTGTTAGGAGACCCCGATAACTACATCCCTGCCAACCCCTCAA
ATACCTTCCCATATCAAGCTGTAAT

Figure 1 a

Sequence of cytochrome b gene (328 bp) revealed from biological material of unknown origin i.e. '*adil.flesh*' using primers '**mcb398**' and '**mcb869**'

Homology search in 'nr' database using 'BLAST'

<http://www.ncbi.nlm.nih.gov/BLAST/>



Sequences producing significant alignments:	Score (bits)	E Value
gb AY005809.1 <i>Panthera pardus</i> cytochrome b gene, partial c...	603	e-170
gb AF053054.1 AF053054 <i>Panthera tigris sumatrae</i> isolate Su1...	527	e-147
gb AF053053.1 AF053053 <i>Panthera tigris tigris</i> isolate B7 mi...	527	e-147
gb AF053050.1 AF053050 <i>Panthera tigris corbetti</i> isolate C2 ...	476	e-132
gb AF053049.1 AF053049 <i>Panthera tigris corbetti</i> isolate C1 ...	476	e-132

Selection of reference animals based on above information
and further analysis using primers '**mcb398**' and '**mcb869**'

Multiple sequence alignments
using 'Autoassembler'

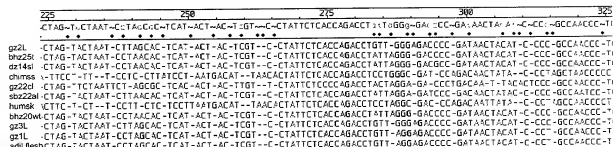


Figure 1 b

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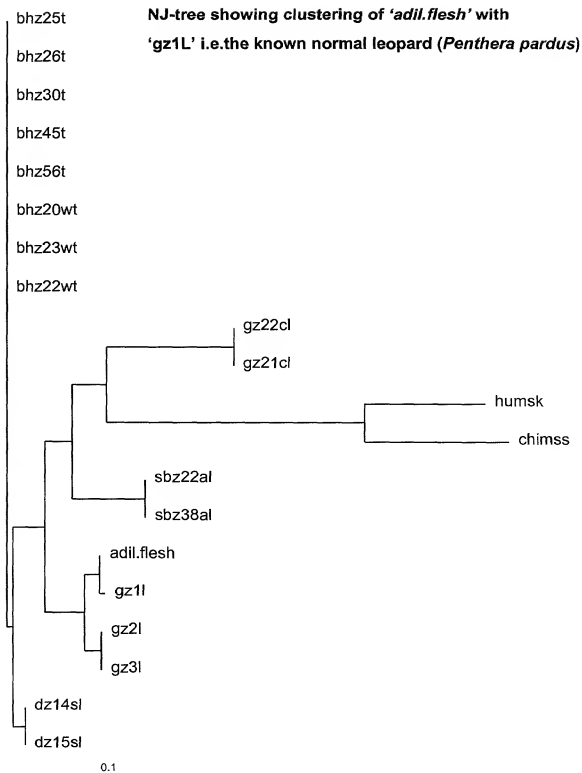


Figure 1c

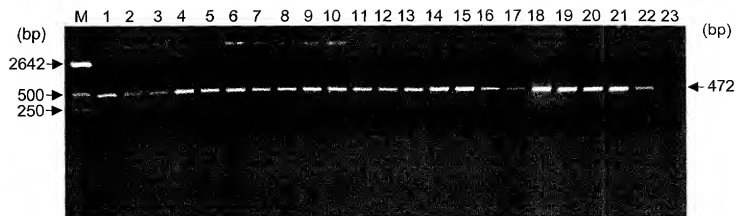


Figure 2



Figure 2

00001742-002001

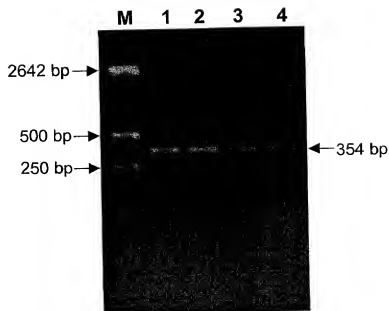


Figure 3

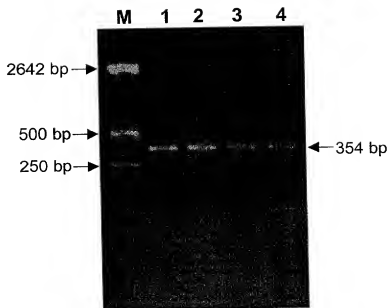


Figure 3



Figure 4

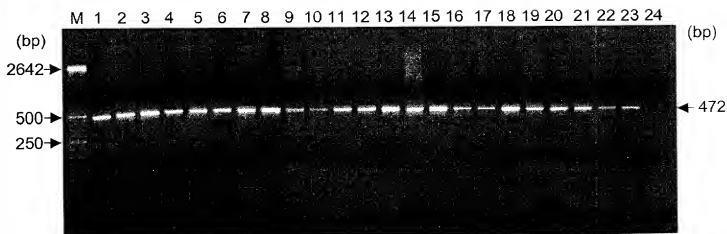


Figure 4